

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/142,471D
Source: 1FW16
Date Processed by STIC: 12/19/05

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IFW16

RAW SEQUENCE LISTING

DATE: 12/19/2005

PATENT APPLICATION: US/09/142,471D

TIME: 09:42:46

Input Set : A:\012627-009.txt

Output Set: N:\CRF4\12192005\I142471D.raw

4 <110> APPLICANT: ROSE-JOHN, Stefan
 5 ANGEWANDTE GENTECHNOLOGIE SYSTEME GMBH
 7 <120> TITLE OF INVENTION: CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN
 PROTEINS

9 <130> FILE REFERENCE: 012627-009
 11 <140> CURRENT APPLICATION NUMBER: 09/142,471D
 12 <141> CURRENT FILING DATE: 1998-11-04
 14 <150> PRIOR APPLICATION NUMBER: PCT/DE97/00458
 15 <151> PRIOR FILING DATE: 1997-03-07
 17 <150> PRIOR APPLICATION NUMBER: DE 196 08 813.5
 18 <151> PRIOR FILING DATE: 1996-03-07
 20 <160> NUMBER OF SEQ ID NOS: 17
 22 <170> SOFTWARE: PatentIn Ver. 2.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1627
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Unknown
 29 <220> FEATURE:
 30 <221> NAME/KEY: sig_peptide
 31 <222> LOCATION: (34)..(90)
 33 <220> FEATURE:
 34 <221> NAME/KEY: mat_peptide
 35 <222> LOCATION: (91)..(1608)
 37 <220> FEATURE:
 38 <221> NAME/KEY: CDS
 39 <222> LOCATION: (34)..(1608)
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Description of Unknown Organism:A conjugate
 43 comprising two polypeptides with a mutual
 44 affinity.
 46 <400> SEQUENCE: 1
 47 gtcgacgcat ggagtggtag ccgaggagga agc atg ctg gcc gtc ggc tgc gcg 54
 48 Met Leu Ala Val Gly Cys Ala
 49 -15
 51 ctg ctg gct gcc ctg ctg gcc gcg ccg gga gcg gcg ctg gcc cca agg 102
 52 Leu Leu Ala Ala Leu Leu Ala Ala Pro Gly Ala Ala Leu Ala Pro Arg
 53 -10 -5 -1 1
 55 cgc tgc cct gcg cag gag gtg gca aga ggc gtg ctg acc agt ctg cca 150
 56 Arg Cys Pro Ala Gln Val Ala Arg Gly Val Leu Thr Ser Leu Pro
 57 5 10 15 20
 59 gga gac agc gtg act ctg acc tgc ccg ggg gta gag ccg gaa gac aat 198
 60 Gly Asp Ser Val Thr Leu Thr Cys Pro Gly Val Glu Pro Glu Asp Asn
 61 25 30 35
 63 gcc act gtt cac tgg gtg ctc agg aag ccg gct gca ggc tcc cac ccc 246

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64 Ala Thr Val His Trp Val Leu Arg Lys Pro Ala Ala Gly Ser His Pro
65          40          45          50
67 agc aga tgg gct ggc atg gga agg agg ctg ctg ctg agg tcg gtg cag 294
68 Ser Arg Trp Ala Gly Met Gly Arg Arg Leu Leu Leu Arg Ser Val Gln
69          55          60          65
71 ctc cac gac tct gga aac tat tca tgc tac cgg gcc ggc cgc cca gct 342
72 Leu His Asp Ser Gly Asn Tyr Ser Cys Tyr Arg Ala Gly Arg Pro Ala
73          70          75          80
75 ggg act gtg cac ttg ctg gtg gat gtt ccc ccc gag gag ccc cag ctc 390
76 Gly Thr Val His Leu Leu Val Asp Val Pro Pro Glu Glu Pro Gln Leu
77 85          90          95          100
79 tcc tgc ttc cgg aag agc ccc ctc agc aat gtt gtt tgt gag tgg ggt 438
80 Ser Cys Phe Arg Lys Ser Pro Leu Ser Asn Val Val Cys Glu Trp Gly
81          105          110          115
83 cct cgg agc acc cca tcc ctg acg aca aag gct gtg ctc ttg gtg agg 486
84 Pro Arg Ser Thr Pro Ser Leu Thr Thr Lys Ala Val Leu Leu Val Arg
85          120          125          130
87 aag ttt cag aac agt ccg gcc gaa gac ttc cag gag ccg tgc cag tat 534
88 Lys Phe Gln Asn Ser Pro Ala Glu Asp Phe Gln Glu Pro Cys Gln Tyr
89          135          140          145
91 tcc cag gag tcc cag aag ttc tcc tgc cag tta gca gtc ccg gag gga 582
92 Ser Gln Glu Ser Gln Lys Phe Ser Cys Gln Leu Ala Val Pro Glu Gly
93          150          155          160
95 gac agc tct ttc tac ata gtg tcc atg tgc gtc gcc agt agt gtc ggg 630
96 Asp Ser Ser Phe Tyr Ile Val Ser Met Cys Val Ala Ser Ser Val Gly
97 165          170          175          180
99 agc aag ttc agc aaa act caa acc ttt cag ggt tgt gga atc ttg cag 678
100 Ser Lys Phe Ser Lys Thr Gln Thr Phe Gln Gly Cys Gly Ile Leu Gln
101          185          190          195
103 cct gat ccg cct gcc aac atc aca gtc act gcc gtg gcc aga aac ccc 726
104 Pro Asp Pro Pro Ala Asn Ile Thr Val Thr Ala Val Ala Arg Asn Pro
105          200          205          210
107 cgc tgg ctc agt gtc acc tgg caa gac ccc cac tcc tgg aac tca tct 774
108 Arg Trp Leu Ser Val Thr Trp Gln Asp Pro His Ser Trp Asn Ser Ser
109          215          220          225
111 ttc tac aga cta cgg ttt gag ctc aga tat cgg gct gaa cgg tca aag 822
112 Phe Tyr Arg Leu Arg Phe Glu Leu Arg Tyr Arg Ala Glu Arg Ser Lys
113          230          235          240
115 aca ttc aca aca tgg atg gtc aag gac ctc cag cat cac tgt gtc atc 870
116 Thr Phe Thr Thr Trp Met Val Lys Asp Leu Gln His His Cys Val Ile
117 245          250          255          260
119 cac gac gcc tgg agc ggc ctg agg cac gtg gtg cag ctt cgt gcc cag 918
120 His Asp Ala Trp Ser Gly Leu Arg His Val Val Gln Leu Arg Ala Gln
121          265          270          275
123 gag gag ttc ggg caa ggc gag tgg agc gag tgg agc ccg gag gcc atg 966
124 Glu Glu Phe Gly Gln Gly Glu Trp Ser Glu Trp Ser Pro Glu Ala Met
125          280          285          290
127 ggc acg cct tgg aca gaa tcc agg agt cct cca gct cga gga ggt gga 1014
128 Gly Thr Pro Trp Thr Glu Ser Arg Ser Pro Pro Ala Arg Gly Gly Gly

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129          295          300          305
131 ggt tct gga ggt gga ggt tct gga ggt gga ggt tct gtc gag cca gta 1062
132 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Val Glu Pro Val
133          310          315          320
135 ccc cca gga gaa gat tcc aaa gat gta gcc gcc cca cac aga cag cca 1110
136 Pro Pro Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro
137 325          330          335          340
139 ctc acc tct tca gaa cga att gac aaa caa att cgg tac atc ctc gac 1158
140 Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp
141          345          350          355
143 ggc atc tca gcc ctg aga aag gag aca tgt aac aag agt aac atg tgt 1206
144 Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys
145          360          365          370
147 gaa agc agc aaa gag gca ctg gca gaa aac aac ctg aac ctt cca aag 1254
148 Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys
149          375          380          385
151 atg gct gaa aaa gat gga tgc ttc caa tct gga ttc aat gag gag act 1302
152 Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr
153          390          395          400
155 tgc ctg gtg aaa atc atc act ggt ctt ttg gag ttt gag gta tac cta 1350
156 Cys Leu Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu
157 405          410          415          420
159 gag tac ctc cag aac aga ttt gag agt agt gag gaa caa gcc aga gct 1398
160 Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala
161          425          430          435
163 gtg cag atg agt aca aaa gtc ctg atc cag ttc ctg cag aaa aag gca 1446
164 Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala
165          440          445          450
167 aag aat cta gat gca ata acc acc cct gac cca acc aca aat gcc agc 1494
168 Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser
169          455          460          465
171 ctg ctg acg aag ctg cag gca cag aac cag tgg ctg cag gac atg aca 1542
172 Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr
173          470          475          480
175 act cat ctc att ctg cgc agc ttt aag gag ttc ctg cag tcc agc ctg 1590
176 Thr His Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu
177 485          490          495          500
179 agg gct ctt cgg caa atg tagcatgggc accgtcgac 1627
180 Arg Ala Leu Arg Gln Met

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181 505

184 <210> SEQ ID NO: 2

185 <211> LENGTH: 525

186 <212> TYPE: PRT

187 <213> ORGANISM: Unknown

189 <220> FEATURE:

190 <223> OTHER INFORMATION: A conjugate comprising two polypeptides with a mutual affinity

192 <400> SEQUENCE: 2

193 Met Leu Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro

194 -15

-10

-5

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196 Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
197      -1  1      5      10
199 Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
200      15      20      25
202 Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
203  30      35      40      45
205 Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
206      50      55      60
208 Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
209      65      70      75
211 Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
212      80      85      90
214 Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
215      95      100      105
217 Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
218 110      115      120      125
220 Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
221      130      135      140
223 Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
224      145      150      155
226 Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
227      160      165      170
229 Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
230      175      180      185
232 Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val
233 190      195      200      205
235 Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp
236      210      215      220
238 Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
239      225      230      235
241 Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
242      240      245      250
244 Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
245      255      260      265
247 Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
248 270      275      280      285
250 Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
251      290      295      300
253 Pro Pro Ala Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
254      305      310      315
256 Gly Gly Ser Val Glu Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val
257      320      325      330
259 Ala Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys
260      335      340      345
262 Gln Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr
263 350      355      360      365
265 Cys Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu
266      370      375      380
268 Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln

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269          385          390          395
271 Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu
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274 Leu Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser
275          415          420          425
277 Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile
278 430          435          440          445
280 Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro
281          450          455          460
283 Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn
284          465          470          475
286 Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys
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289 Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
290          495          500          505
293 <210> SEQ ID NO: 3
294 <211> LENGTH: 1612
295 <212> TYPE: DNA
296 <213> ORGANISM: Unknown
298 <220> FEATURE:
299 <221> NAME/KEY: sig_peptide
300 <222> LOCATION: (34)..(90)
302 <220> FEATURE:
303 <221> NAME/KEY: CDS
304 <222> LOCATION: (34)..(1593)
306 <220> FEATURE:
307 <221> NAME/KEY: mat_peptide
308 <222> LOCATION: (91)..(1593)
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Description of Unknown Organism:A conjugate
312 comprising two polypeptides with a mutual
313 affinity.
315 <400> SEQUENCE: 3
316 gtcgacgcat ggagtggtag ccgaggagga agc atg ctg gcc gtc ggc tgc gcg 54
317          Met Leu Ala Val Gly Cys Ala
318          -15
320 ctg ctg gct gcc ctg ctg gcc gcg ccg gga gcg gcg ctg gcc cca agg 102
321 Leu Leu Ala Ala Leu Leu Ala Ala Pro Gly Ala Ala Leu Ala Pro Arg
322          -10          -5          -1 1
324 cgc tgc cct gcg cag gag gtg gca aga ggc gtg ctg acc agt ctg cca 150
325 Arg Cys Pro Ala Gln Glu Val Ala Arg Gly Val Leu Thr Ser Leu Pro
326 5          10          15          20
328 gga gac agc gtg act ctg acc tgc ccg ggg gta gag ccg gaa gac aat 198
329 Gly Asp Ser Val Thr Leu Thr Cys Pro Gly Val Glu Pro Glu Asp Asn
330          25          30          35
332 gcc act gtt cac tgg gtg ctc agg aag ccg gct gca ggc tcc cac ccc 246
333 Ala Thr Val His Trp Val Leu Arg Lys Pro Ala Ala Gly Ser His Pro
334          40          45          50
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VERIFICATION SUMMARY

DATE: 12/19/2005

PATENT APPLICATION: US/09/142,471D

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